

CD4: 55%

>ref|NP\_000607.1| CD4 antigen precursor [Homo sapiens]

Length=458

GENE ID: 920 CD4 | CD4 molecule [Homo sapiens] (Over 100 PubMed links)

Score = 459 bits (1181), Expect = 2e-129

Identities = 249/450 (55%), Positives = 314/450 (69%), Gaps = 8/450 (1%)

Query 9 rllllllqlsqliAVTQGKTLVLGKEGESAEPLCESSQKKITVFTWKFSQQRKILGQHCK 68  
R LLL+LQL+ L A TQCK +VLGK+G++ EL C +SQKK F WK S+Q KILG G  
Sbjct 8 RHLLLVQLLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGS 67

Query 69 GVLIRGCGSPSQFDRFDSKKGAWEKGSFPLIINKLKMEDSQTIVICELNRKEEVELWVFKV 128  
+ G DR DS++ W++G+FPLII LK+EDS TYICE+E++KEEV+L VF +  
Sbjct 68 --FLTGPKSKLNDRADSRRLWDQGNFPLIINKLKIEDSDTYICEVEDQKEEVQLLVFGL 125

Query 129 TFSPTgtsllqgqsltltlDSNSKVSNNPLTECKHkkgkvsvsgskvLSMSNLRVQDSDFWNC 188  
T + T LLQGGSLTLTL+S S+P +C+ +GK + G K LS+S L +QDS W C  
Sbjct 126 TANSDTHLLQGGSLTLTLESPPG-SSPSVQCRSPRGKNIQGGKTLVSQLELQDSGTWTC 184

Query 189 TVTLDQKKNWFGMTLSVLGFQSTAITAYKSEGESAEFSFPLNFAEEN--GWGELMWKA EK 246  
TV +QKK F + + VL FQ + YK EGE EFSFPL F E G GEL W+AE+  
Sbjct 185 TVLQNQKKVEFKIDIVLAFQKASSIVYKKEGEQVEFSFPLAFTVEKLTGSGELWWQAER 244

Query 247 DSFFQPWISFSIKNKEVSVQKSTDKLKLQKETLPLTLKIPQVSLQFAGSGNLTLDK- 305  
S + WI+F +KNKEVSV++ T+D KLQ+ + LPL L +PQ Q+AGSGNLT L+  
Sbjct 245 ASSSKSWITFDLKNKEVSVKRVTDQPKLQMGKKLPLHLTLPLQALPQYAGSGNLTALAEAK 304

Query 306 -GTLHQEVNVLVVMKVAQLNNTLTCEVMGPTSPKMRLTLKQENQEARVSEEQKVQVVAPE 364  
G LHQEVNVLVM+ QL LTCEV GPTSPK+ L+LK EN+EA+VS+ +K V V+ PE  
Sbjct 305 TGKLHQEVNVLVVMRATQLQKNLTCEVWGPTSPKMLSLKLENKAKVSKREKAVVVLNPE 364

Query 365 TGLWQCLLSEGDVKVMDSRIQVLSRGVNQTVFLA-CVlggsfgflgflglcilccVRCRH 423  
G+WQCLLS+ +V ++S I+VL +A VLGG G L F+GL I CVRCRH  
Sbjct 365 AGMWQCLLSDSGQVLLESNIKVLPTWSTPVQPMALIVLGGVAGLLLFIFGLGIFFCVRCRH 424

Query 424 QQRQAARMSQIKRLLSEKKTQCPCPHRMQKS 453  
++RQA RMSQIKRLLSEKKTQCPCPHR QK+  
Sbjct 425 RRRQAARMSQIKRLLSEKKTQCPCPHRFQKT 454



Her2: 87%

GENE ID: 2064 ERBB2 | v-erb-b2 erythroblastic leukemia viral oncogene homolog  
2, neuro/glioblastoma derived oncogene homolog (avian) [Homo sapiens]  
(Over 100 PubMed links)

Score = 2308 bits (5981), Expect = 0.0

Identities = 1101/1256 (87%), Positives = 1156/1256 (92%), Gaps = 1/1256 (0%)

Query 1	MELAAWCRWGFLLALLSPGAAGTQVCTGTDMLRLPASPETHDMLRHLYQGCQVVGQNL	60
	MELAA CRWG LLALL PGAA TQVCTGTDMLRLPASPETHDMLRHLYQGCQVVGQNL	
Sbjct 1	MELAALCRWGLLLALLPPGAASTQVCTGTDMLRLPASPETHDMLRHLYQGCQVVGQNL	60
Query 61	ELTYLPANASLSFLQDIQEVQGYMLIAHNRVKHVPLQRLRIVRGTLFEDKYALAVLDNR	120
	ELTYLP NASLSFLQDIQEVQGY+LIAHN+V+ VPLQRLRIVRGTLFED YALAVLDN	
Sbjct 61	ELTYLPTNASLSFLQDIQEVQGYVLIAHNQVRQVPLQRLRIVRGTLFEDNYALAVLDNG	120
Query 121	DPLDNVTTAAPGRTPEGLRELQLRSLTEILKGGVLRGNPQLCYQDMVLWKDVLKNNQL	180
	DPL+N TT G +P GLRELQLRSLTEILKGGVLI+ NPQLCYQD +LWKD+ KNNQL	
Sbjct 121	DPLNN-TTPVTGASPGGLRELQLRSLTEILKGGVLIQRNPQLCYQDTILWKDIFHKNNQL	179
Query 181	APVMDTNRSRACPPCAPTCKDNHCWGESPEDCQILTGTICTSGCARCKGRLPTDCCHEQ	240
	A +DTNRSRAC PC+P CK + CWGES EDCQ LT T+C GCARCKG LPTDCCHEQ	
Sbjct 180	ALTLDITNRSRACHPCSPMCKGSRWCWGESSEDCQSLTRTVCAGGCARCKGPLPTDCCHEQ	239
Query 241	CAAGCTGPKHSDCLACLHFNHSGICELHCPALITYNTDTFESMLNPEGRYTFGASCVTTC	300
	CAAGCTGPKHSDCLACLHFNHSGICELHCPAL+TYNTDTFESM NPEGRYTFGASCVT C	
Sbjct 240	CAAGCTGPKHSDCLACLHFNHSGICELHCPALVITYNTDTFESMPNPEGRYTFGASCVTAC	299
Query 301	PYNYLSTEVGSCTLVCPNNQEVTAEDGTQRCEKCSKPCAGVCYGLGMEHLRGARAITSD	360
	PYNYLST+VGSCTLVCP +NQEVTAEDGTQRCEKCSKPCA VCYGLGMEHLR RA+TS	
Sbjct 300	PYNYLSTDVGSCTLVCPLNHNEVTAEDGTQRCEKCSKPCARVCYGLGMEHLREVRAVTS	359
Query 361	NIQEFAGCKKIFGSLAFLPESFDGNPSSGVAPLKPEHLQVFETLEEITGYLYISAWPESF	420
	NIQEFAGCKKIFGSLAFLPESFDG+P+S APL+PE LQVFETLEEITGYLYISAWP+S	
Sbjct 360	NIQEFAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETLEEITGYLYISAWPSL	419
Query 421	QDLSVFQNLRVIRGRILHDGAYSLTLQGLGIHslglrsrlrelgsglaliHRNTHLCFVNT	480
	DLSVFQNL+VIRGRILH+GAYSLTLQGLGI LGLRSLRELGSGLALIH NTHLCFV+T	
Sbjct 420	PDLSVFQNLQVIRGRILHNGAYSLTLQGLGISWLGLRSLRELGSGLALIIHNTHLCFVHT	479
Query 481	VPWDQLFRNPHQALLHSGNRPEEACGLEGLVCNSLCARGHCWGPPTQCVNCSQFLRGQE	540
	VPWDQLFRNPHQALLH+ NRPE+ C EGL C+ LCARGHCWGPPTQCVNCSQFLRGQE	
Sbjct 480	VPWDQLFRNPHQALLHTANRPEDECVGEGLACHQLCARGHCWGPPTQCVNCSQFLRGQE	539
Query 541	CVEECRVWKGLPREYVRGKHCLPCHPECQPQNSSETCYGSEADQCEACAHYKDSSECVAR	600
	CVEECRV +GLPREYV +HCLPCHPECQPQN S TC+G EADQC ACAHYKD CVAR	
Sbjct 540	CVEECRVLQGLPREYVNARHCLPCHPECQPQNGSVTCFGEADQCVACAHYKDPFPCVAR	599
Query 601	CPSGVKPDLSYMPIWKYPDEEGICQPCPINCTHSCVDLDERGCPAEQRASPVTFIIATvv	660
	CPSGVKPDLSYMPIWK+PDEEG CQPCPINCTHSCVDLD++GCPAEQRASP+T II+ VV	
Sbjct 600	CPSGVKPDLSYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTSIISAVV	659
Query 661	gvllfliivvvigilikrrrqkirkYTMRRLLQETELVEPLTPSGAVPNQAQMRILKETE	720

Sbjct	660	G+LL +++ VV GILIKRR+QKIRKYTMRRLLQETELVEPLTPSGA+PNQAQMRILKETE GILLVVVLGVVFGILIKRRQKIRKYTMRRLLQETELVEPLTPSGAMPNQAQMRILKETE	719
Query	721	LRKLKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVGS LRK+KVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVGS	780
Sbjct	720	LRKVKVLGSGAFGTVYKGIWIPDGENVKIPVAIKVLENTSPKANKEILDEAYVMAGVGS	779
Query	781	PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVREHGRGLGSQDLLNWCVQIAKCMSYLEEV PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRE+RGRLGSQDLLNWC+QIAKCMSYLE+V	840
Sbjct	780	PYVSRLLGICLTSTVQLVTQLMPYGCLLDHVRENCRGLGSQDLLNWCQIAKCMSYLEDV	839
Query	841	RLVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPIKWMALLESILRRRF RLVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPIKWMALLESILRRRF	900
Sbjct	840	RLVHRDLAARNVLKSPNHVKITDFGLARLLDIDETEHADGGKVPIKWMALLESILRRRF	899
Query	901	THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYIMVVKCW THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYIMVVKCW	960
Sbjct	900	THQSDVWSYGVTVWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICTIDVYIMVVKCW	959
Query	961	MIDSECRPRFRELVSFMRMARDPQRFVVIQNEDLGPSSPMDSTFYRSLEDDDMGELVD MIDSECRPRFRELVSFMRMARDPQRFVVIQNEDLGP+SP+DSTFYRSLEDDDMG+LVD	1020
Sbjct	960	MIDSECRPRFRELVSFMRMARDPQRFVVIQNEDLGPASPLDSTFYRSLEDDDMGDLVD	1019
Query	1021	AEEYLVPQQGFFSPDPALGtgstahrrhrssarsgggeltlglepseepprsplapse AEEYLVPQQGFF PDPA G G H RHRSSS RSGGG+LTGLGPSEEE PRSPLAPSE	1080
Sbjct	1020	AEEYLVPQQGFFCPDPAPGAGGMVHHRSSSTRSGGGDLTLGLPSEEEAPRSPLAPSE	1079
Query	1081	GAGSDVFDGDLAVGVTGKLQSLSPHDLSPQRYSEDPTLPLPPETDGYVAPLACSPQPEY GAGSDVFDGDL +G KGLQSL HD SPLQRYSEDPT+PLP ETDGYVAPL CSPQPEY	1140
Sbjct	1080	GAGSDVFDGDLGMGAAGKLQSLPTHDPSPQRYSEDPTVPLPSETDGYVAPLTCSPQPEY	1139
Query	1141	VNQPEVRpqspltpgppppirpAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLAP VNQP+VRPQ P EGP P RPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYL P	1200
Sbjct	1140	VNQPDVRPQPPSPREGPLPAARPAGATLERPKTLSPGKNGVVKDVFAFGGAVENPEYLTP	1199
Query	1201	RAGTASQPHPSPAFSPAFDNLYYWDQNSSEQGPPPTFEGTPTAENPEYLGLDVPV + G A QPHP PAFSPAFDNLYYWDQ+ E+G PPSTF+GTPTAENPEYLGLDVPV	1256
Sbjct	1200	QGGAAPQPHPPAFSPAFDNLYYWDQDPPPERGAPPSTFKGTPTAENPEYLGLDVPV	1255

CD80: 45%

>ref|NP\_005182.1| CD80 antigen precursor [Homo sapiens]

Length=288

GENE ID: 941 CD80 | CD80 molecule [Homo sapiens] (Over 10 PubMed links)

Score = 228 bits (581), Expect = 5e-60

Identities = 124/271 (45%), Positives = 171/271 (63%), Gaps = 6/271 (2%)

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Query 18  CPrlillfvllir-lSQVSSDVDEQLSKSVKDKVLLPCRYNSPHEDESEDRIYWQKHDKV 76
          CP L   +L++ LS  S V  ++K VK+  L C +N  E+ ++ RIYWQK  K+
Sbjct 14  CPYLNFFQLLVLAGLSHFCSGVIH-VTKEVKEVATLSCGHNVSVVEELAQTRIYWQKEKKM 72

Query 77  VLSVIAGKLVWPEYKNRTLYDNTT-YSLIILGLVLSDRGTYSVQVQKKERGTYEVKHLA 135
          VL+++G + +WPEYKNRT++D T   S++IL L  SD GTY CVV K E+  ++ +HLA
Sbjct 73  VLTMMSGDMNIWPEYKNRTIFDITNLSIVILALRPSDEGTYECVVLKYEKDAFKREHLA 132

Query 136 LVKLSIKADFSTPNITESGNPSADTKRITCFASGGFPKPRFSWLENGRELPGINTTISQD 195
          V LS+KADF TP+I++  P+++ +RI C  SGGFP+P  SWLENG EL  INTT+SQD
Sbjct 133 EVTLSVKADFPTPSISDFEIPTSNIRRIICSTSGGFPEPHLSWLENGEELNAINTTVSQD 192

Query 196 PESELYTISSQLDFNTTRNHTIKCLIKYGDAHVSEDFTWEKPPEDP-PDSKNTLVLFAGAG 254
          PE+ELY +SS+LDFN T NH+ CLIKYG  V++ F W  ++ PD N L  +
Sbjct 193 PETELYAVSSKLDNMTTNHSMCLIKYGHLRVNQTFNWNTTKQEHFPD--NLLPSWAIT 250

Query 255 FGAvitvvvivviiKCFCKHRSCFRRNEASR 285
          +V + VI + CF      RRNE R
Sbjct 251 LISVNGIFVICCLTYCFAPRCRERRRNERLR 281
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CD86: 50%

>ref|NP\_787058.3| CD86 antigen isoform 1 [Homo sapiens]

Length=329

GENE ID: 942 CD86 | CD86 molecule [Homo sapiens] (Over 10 PubMed links)

Score = 287 bits (734), Expect = 9e-78

Identities = 154/305 (50%), Positives = 198/305 (64%), Gaps = 9/305 (2%)

```
Query 1  MDPRCTMGLAILIFVTVLLISDAVSQAYFNGTAYLPCPFTKAQNISLSELVVFWDQ 60
      MDP+CTMGL+ ++FV  L+S A  ++ QAYFN TA LPC F  +QN SLSELVVFWDQ
Sbjct 1  MDPQCTMGLSNILFVMAFLLSGAAPLKIQAYFNETADLPCQFANSQNSLSELVVFWDQ 60

Query 61  QKLVLVEHYLGTEKLDVNAKYLGRTSFDRNNWTLRLHNVQIKDMGSYDCFIQKKPPTGS 120
      + LVL E YLG EK DSV++KY+GRTSFD ++WTLRLHN+QIKD G Y C I  K PTG
Sbjct 61  ENLVLNEVYLGKEKFDVSHSKYMGRTSFDSDSWTLRLHNLQIKDKGLYQCIIHKKPTGM 120

Query 121  IILQQTLTELSVIANFSEPEIKLAQNVGTGNSGINLTCTSKQGHKPKKMYFLI--TNSTN 178
      I + Q  +ELSV+ANFS+PEI  N+T N  INLTC+S  G+P+PKKM  L+  NST
Sbjct 121  IRIHQMNSELSVLANFSQPEIVPISNITENVYINLTCSSIHGYPEPKMSVLLRTKNSTI 180

Query 179  EYGDNMQISQDNVTelfsisnslsfPDGVWHMTVVCVLETESMKISSKPLNFTQEFPS 238
      EY  MQ SQDNVTEL+ +S SLS+SFPD  +MT+ C+LET+  ++ S P +  E P
Sbjct 181  EYDGVMQSQDNVTelydvsislsvsfpdvtsnmtifciletdktrllsppfsieleDPQ 240

Query 239  P---QTYWKEitasvtvallvmllivCHKKPNQPSRP-----SNTASKLERDSNADRET 291
      P      W      +  ++V LI+  KK  +P      +NT  + E +  RE
Sbjct 241  PPPDHPWITAVLPTVIIICVMVFCLILWKKKKKRPRNSYKCGTNTMERESEQTKKREK 300

Query 292  INLKE 296
      I++ E
Sbjct 301  IHIFE 305
```

CD28: 69%

>ref|NP\_006130.1| CD28 antigen [Homo sapiens]  
Length=220

GENE ID: 940 CD28 | CD28 molecule [Homo sapiens] (Over 100 PubMed links)

Score = 297 bits (760), Expect = 5e-81

Identities = 152/219 (69%), Positives = 171/219 (78%), Gaps = 5/219 (2%)

```
Query 3  LRLFLALNFF-SVQVTENKILVKQSPLLVVDSNEVSLSCRYSYNLLAKEFRASLYKGVN 61
          LRL LALN F S+QVT NKILVKQSP+LV N V+LSC+YSYNL ++EFRASL+KG++
Sbjct 2  LRL-LALNLFPSIQVTGNKILVKQSPMLVAYDNAVNLSCKYSYNLFSREFRASLHKGLD 60

Query 62 SDVEVCVGNGNFTYQPQFRSNAEFNCDGDFDNETVTFRNLHVNHTDIYFCKIEFMYPP 121
          S VEVCV GN++ Q Q S FNC DG NE+VTF L NL+VN TDIYFCKIE MYPP
Sbjct 61 SAVEVCVVGNYSQLQVYSKTGFNCDGKLGNESVTFYLQNLVYNQTDIYFCKIEVMYPP 120

Query 122 PYLDNERSNGTIIHIKEKHLCHTQSSP---KLFWALVVVAGVLFYGLLVTVLVCVIWTN 178
          PYLDNE+SNGTIIH+K KHL C + P K FW LVVV GVL CY LLVTVA + W
Sbjct 121 PYLDNEKSGTIIHVKGKHLCPSPFPGPSKPFWWLVVVGVLACYSLLVTVAFIIFWVR 180

Query 179 SRRNRLLQSDYMNMTPRRPGLTRKPYQPYAPARDFAAAYR 217
          S+R+RLL SDYMNMTPRRPG TRK YQPYAP RDFAAAYR
Sbjct 181 SKRSRLLHSDYMNMTPRRPGPTRKHVQPYAPPRDFAAAYR 219
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CD70: 56%

>ref|NP\_001243.1| tumor necrosis factor ligand superfamily, member 7 [Homo sapiens]  
Length=193

GENE ID: 970 CD70 | CD70 molecule [Homo sapiens] (Over 10 PubMed links)

Score = 195 bits (495), Expect = 2e-50

Identities = 110/195 (56%), Positives = 124/195 (63%), Gaps = 2/195 (1%)

```
Query 1  MPEEGRPCPWVRWSGTAFQRQWPWLLLVVFITVFCCWFHCSGLLSKQQQRLEHPEPHTA 60
          MPEEG C R R L+ +V V C QQQ LE A
Sbjct 1  MPEECGCSVRRRPYGCVLRAA--LVPLVAGLVICLVVCIQRFQAQQQLPLESLGWDVA 58

Query 61 ELQLNLTVPKRDPTLRWGAGPALGRSFTHGPELEEGLRIHQDGLYRLHIQVTLANCSSP 120
          ELQLN T P++DP L W GPALGRSF HGPEL++G LRIH+DG+Y +HIQVTLA CSS
Sbjct 59 ELQLNHTGPQQDPRLYWQGGPALGRSFLHGPELDKGQLRIHRDGIYMVHIQVTLAICSST 118

Query 121 GSTLQHRATLAVGICSPAAHGISLLRGRFGQDCTVALQRLTYLVHGDVLTNLTLPLPS 180
          ++ H TLAVGICSPA+ ISLLR F Q CT+A QRLT L GD LCTNLT LLPS
Sbjct 119 TASRHHPTTLAVGICSPASRSISLLRLSFHQGCTIASQRLTPLARGDTLCTNLTGTLLPS 178

Query 181 RNADETFFGVQWICP 195
          RN DETFFGVQW+ P
Sbjct 179 RNTDETFFGVQWVRP 193
```

CD11b: 70%

>ref|NP\_000623.2| integrin alpha M precursor [Homo sapiens]

Length=1152

GENE ID: 3684 ITGAM | integrin, alpha M (complement component 3 receptor 3 subunit) [Homo sapiens] (Over 100 PubMed links)

Score = 1765 bits (4571), Expect = 0.0

Identities = 863/1153 (74%), Positives = 1003/1153 (86%), Gaps = 1/1153 (0%)

Query	1	MtlkallvtalalCHGFNLDTEHPMTFQENAKGFGQSVVQLGGTSVVVAAPQEAKAVNQT	60
		M L+ LL+TAL LCHGFNLDTE+ MTFQENA+GFGQSVVQL G+ VVV APQE A NQ	
Sbjct	1	MALRVLLLTALTLCCHGFNLDTENAMTFQENARGFGQSVVQLQGSRVVVGAPQEIVANQR	60
Query	61	GALYQCDYSTSRCHPIPLQVPPEAVNMSLGLSLAVSTVPQQLACGPTVHQNCENTYVN	120
		G+LYQCDYST C PI LQVP EAVNMSLGLSLA +T P QLLACGPTVHQ C ENTYV	
Sbjct	61	GSLYQCDYSTGSCPIRLQVPVEAVNMSLGLSLAATTSPPQQLACGPTVHQTCSENTYVK	120
Query	121	GLCYLFGSNLLRPPQQFPEALRECPQESDIVFLIDSGSINNIDFQKMKEFVSTVMEQF	180
		GLC+LFGSNL + PQ+FPEALR CPQ++SDI FLIDSGSI DF++MKEFVSTVMEQ	
Sbjct	121	GLCFLFGSNLRQQPQKFPEALRGCPQEDSDIAFLIDSGSIIPHDFRRMKEFVSTVMEQL	180
Query	181	KKSKTLFSLMQYSDEFRIHFTFNDFKRNPSPRSHVSPKQLNGRTKTASGIRKVVRELFH	240
		KKSKTLFSLMQYS+EFRIHFTF +F+ NP+PRS V PI QL GRT TA+GIRKVVRELF+	
Sbjct	181	KKSKTLFSLMQYSEEFRIHFTFKEFQNNPNPRSLVKPITQLLGRTHATGIRKVVRELFN	240
Query	241	KTNGARENAKILVVITDGEKFGDPLDYKDVPEADRAGVIRYVIGVGNFNPQSRREL	300
		TNGAR+NA KILVVITDGEKFGDPL Y+DVPEADR GVIRYVIGV+AF +SR+EL	
Sbjct	241	ITNGARKNAFKILVVITDGEKFGDPLGYEDVPEADREGVIRYVIGVGDARSEKSRQEL	300
Query	301	DTIASKPAGEHVQVDNFEALNTIQNLQEKIFAIEGTQTGTSSTFEHEMSQEGFSASIT	360
		+TIASKP +HVQV+NFEAL TIQNQL+EKIFAIEGTQTGS+SSFEHEMSQEGFSA+IT	
Sbjct	301	NTIASKPPRDHVQVNNFEALKTIQNQLREKIFAIEGTQTGSSSTFEHEMSQEGFSAAIT	360
Query	361	SNGPLLGSVGSFWDWAGGFLYTSKDKVTFINTTRVDSMDNDAYLGYASAVILNRNVQSLV	420
		SNGPLL +VGS+DWAGG FLYTSK+K TFIN TRVDSMDNDAYLGYA+A+ILNRNVQSLV	
Sbjct	361	SNGPLLSTVGSYDWAGGVFLYTSKEKSTFINMTRVDSMDNDAYLGYAAIILNRNVQSLV	420
Query	421	LGAPRYQHIGLVVMFRENFGTWEPHTSIKGSQIGSYFGASLCSVDMADGNTNLILIGAP	480
		LGAPRYQHIGLV MFR+N G WE + ++KG+QIG+YFGASLCSVD+D++G+T+L+LIGAP	
Sbjct	421	LGAPRYQHIGLVAMFRQNTGMWESNANVKGTQIGAYFGASLCSVDVDSNGSTDLLVIGAP	480
Query	481	HYYEKTRGGQVSVCPPLPRGRARWQCEALLHGDQGHWPGRFGAALTVLGDVNGDKLTDVAI	540
		HYYE+TRGGQVSVCPPLPRGRARWQC+A+L+G+QG PWGRFGAALTVLGDVNGDKLTDVAI	
Sbjct	481	HYYEKTRGGQVSVCPPLPRGRARWQCDVLYGEQQGPWGRFGAALTVLGDVNGDKLTDVAI	540
Query	541	GAPGEQENQGAUVYIFYGASIASLSASHSQRIIGAHSFPLQYFGQSLSGGKDLTMDGLMD	600
		GAPGE++N+GAUVY+F+G S + +S SHSQRI G+ SP LQYFGQSLSGG+DLTMDGL+D	
Sbjct	541	GAPGEEDNRGAUVLFHGTSGSGISPSHSQRIAGSKLSPRLQYFGQSLSGGQDLTMDGLVD	600
Query	601	LAVGAQGHilllraqpvlriEATMEFSPKKVARSVFACQEQVLKNKDAGEVRVCLRVKRN	660
		L VQAQGH+LLLR+QPVL++A MEF+P++VAR+VF C +QV+K K+AGEVRVCL V+K+	
Sbjct	601	LTVGAQGHVLLRSQPVLRVKAIIEFNPREVARNVFECNDQVVKGEAGEVRVCLHVQKS	660



Query	661	TKDRLREGDIQSTVTYDLALDPGRSRIRAFFDETKNNTRRRRTQVFGLMQKCETLKLILPD	720
		T+DRLREG IQS VTYDLALD GR RA F+ETKN+TRR+TQV GL Q CETLKL LP+	
Sbjct	661	TRDRLREGQIQSVVTYDLALDSGRPHSRVFNETKNSTRRQTQVLGLTQTCETLKLQLPN	720
Query	721	CVDDSVSPIIILRLNYTLVGEPLRSFGNLRPVLAMDAQRFFTAMFPFEKNCGNDSICQDDL	780
		C++D VSPI+LRLN++LVG PL +FGNLRPVLA DAQR FTA+FPFEKNCGN+ICQDDL	
Sbjct	721	CIEDPVSPIVLRLNFSLVGTPLSAFGNLRPVLAEDAQRLFTALFPFEKNCGN+ICQDDL	780
Query	781	SITMSAMGLDTLVVGGPQDFNMSVTLRNDGEDSYGTQVTVYYPSGLSYRKDSASQNPLTK	840
		SIT S M LD LVVGGP++FN++VT+RNDGEDSY TQVT ++P LSYRK S QN ++	
Sbjct	781	SITFSMSLDCLLVGGPREFNVTVTVRNDGEDSYRTQVTFFFLDLSYRKVSTLQNRSQ	840
Query	841	KPWFVKPAessssseGHGALKSTTWNINHIPIFANSEVTFNVTDFVDSHASFGNKLLKA	900
		+ W + ES+SS+E GALKST+ +INHPIFP NSEVTFN+TFDVDS AS GNKLLKA	
Sbjct	841	RSWRL-ACESASSTEVSGALKSTSCSINHPIFPENSEVTFNITFDVDSKASLGNKLLKA	899
Query	901	IVASENNMSRTHKTKFQLELPVKYAIYMIVTSDESSIRYLNFTASEMTSKVIQHQQFNN	960
		V SENNM RT+KT+FQLELPVKYA+YM+VTS S +YLNFTASE TS+V+QHQQ +N	
Sbjct	900	NVTSENNMPRTNKTEFQLELPVKYAVYMVVTSHGVS TKYLNFTASENSTRVMQHQQVSN	959
Query	961	LGQRSLPVSVFWIPVQINNVTVDHPQVIFSQNLSSACHTEQKSPPHSNFRDQLERTPV	1020
		LGQRSLP+S+VF +PV++N +WD PQV FS+NLSS CHT+++ P HS+F +L + PV	
Sbjct	960	LGQRSLPISLVFLVPVRLNQTVIWRPQVTFSENLSSTCHTKERLP SHSDFLAELRKAPV	1019
Query	1021	LNCSYAVCKRIQCDLPSFNTQEIFNVTLKGNSFDWYIKTSHGHLLLVSSTEILFNDSAF	1080
		+NCS+AVC+RIQCD+P F QE FN TLKGNSFDWYIKTSH HLL+VS+ EILFNDS F	
Sbjct	1020	VNCSIAVCQRIQCDIPFFGIQEEFNATLKGNSFDWYIKTSHNHLIVSTAEILFNDSVF	1079
Query	1081	ALLPGQESYVRSKTETKVEPYEVHNPVPLIVGSSIGGLVLLALITAGLYKLGFVKRQYKD	1140
		LLPGQ ++VRS+TETKVEP+EV NP+PLIVGSS+GGL+LLALITA LYKLGFVKRQYKD	
Sbjct	1080	TLLPGQGA FVRSQTETKVEPFEVNPPLPLIVGSSVGGLLLALITAALYKLGFVKRQYKD	1139
Query	1141	MMNEAAPQDAPPQ	1153
		MM+E P A PQ	
Sbjct	1140	MMSEGGPPGAEPQ	1152

CD18: 81%

>ref|NP\_000202.2| integrin, beta 2 precursor [Homo sapiens]  
Length=769

GENE ID: 3689 ITGB2 | integrin, beta 2 (complement component 3 receptor 3 and 4 subunit) [Homo sapiens] (Over 100 PubMed links)

Score = 1351 bits (3497), Expect = 0.0

Identities = 632/771 (81%), Positives = 694/771 (90%), Gaps = 2/771 (0%)

```
Query 1  MlglrpslllalaglfflgsaVSQECTKYKVSSCRDCIQSGPGCSWCQKLNFTGPGEPPDS 60
          MLGLRP LL AL GL LG +SQECHK+KVSSCR+CI+SGPGC+WCQKLNFTGPG+PDS
Sbjct 1  MLGLRPPLL-ALVGLLSLGCVLVSQECTKFKVSSCRECIESGPGCTWCQKLNFTGPGDPDS 59

Query 61  LRCDTRAQLLLKCPADDIMDPRSIANPEFDQGRQKQLSPQKVTLYLPGQAAAFNVTF 120
          +RCDTR QLL++GC ADDIMDP S+A + D G +KQLSPQKVTLYLPGQAAAFNVTF
Sbjct 60  IRCDTRPQLLMRGCAADDIMDPTSLAETQEDHNGGQKQLSPQKVTLYLPGQAAAFNVTF 119

Query 121  RRAKGYPIdlylmdlsysmlddINNKKLGGDLLQALNEITESGRIGFGSFVDKTVLPF 180
          RRAKGYPIDLYYLMDSYSMLDDL NVKKLGGDLL+ALNEITESGRIGFGSFVDKTVLPF
Sbjct 120  RRAKGYPIDLYYLMDSYSMLDDLNRVKKLGGDLLRALNEITESGRIGFGSFVDKTVLPF 179

Query 181  VNTHPEKLRNPCPNKEKACQPPFAFRHVLKLTDNSNQFQTEVGKQLISGNLDAPEGGLDA 240
          VNTHP+KL RNPCPNKEK CQPPFAFRHVLKLT+NSNQFQTEVGKQLISGNLDAPEGGLDA
Sbjct 180  VNTHPKLRNPCPNKEKECQPPFAFRHVLKLTNNSNQFQTEVGKQLISGNLDAPEGGLDA 239

Query 241  IMQVAACPEEIGWRNVTRLLVFATDDGFHFAGDGKLGAILTPNDGRCHLEDNMYKRSNEF 300
          +MQVAACPEEIGWRNVTRLLVFATDDGFHFAGDGKLGAILTPNDGRCHLEDN+YKRSNEF
Sbjct 240  MMQVAACPEEIGWRNVTRLLVFATDDGFHFAGDGKLGAILTPNDGRCHLEDNLYKRSNEF 299

Query 301  DYPSVGQLAHKLSESNIQIPFAVTKKMVKTYEKLTEIIPKSAVGELSDDSSNVVQLIKNA 360
          DYPSVGQLAHKL+E+NIQIPFAVT +MVKTYEKLTEIIPKSAVGELS+DSSNVVQLIKNA
Sbjct 300  DYPSVGQLAHKLAENNIQIPFAVTSRMVKTYEKLTEIIPKSAVGELSEDSSNVVQLIKNA 359

Query 361  YYKLSSRVFLDHSTLPDTLKVTYDSFCSNGASSIGKSRGDCDGVQINNPVTFQVKVMASE 420
          Y KLSSRVFLDH+ LPDTLKVTYDSFCSNG + + RGDCDGVQIN P+TFQVKV A+E
Sbjct 360  YNKLSSRVFLDHNALPDTLKVTYDSFCSNGVTHRNQPRGDCDGVQINVPITFQVKVTATE 419

Query 421  CIQEQS FVIRALGFTDVTVTQVRPQCECQCRDQSRQSLCGGKGVMECGICRCESGYIGK 480
          CIQEQS FVIRALGFTD VTVQV PQCEC+CRDQSR++SLC GK +ECGICRC++GYIGK
Sbjct 420  CIQEQS FVIRALGFTDIVTVQVLPQCECQCRDQSRDRSLCHGKGFLECGICRCDTGYIGK 479

Query 481  NCECQTQGRSSQELERNCRKDNSSIIVCSGLGDCICGQCVCHTSDVPNKEIFGQYCECDNV 540
          NCECQTQGRSSQELE +CRKDN+SI+CSGLGDC+CGQC+CHTSDVP K I+GQYCECD +
Sbjct 480  NCECQTQGRSSQELGSCRKDNSSIICSGLGDCVCGQCLCHTSDVPKLIYQYCECDTI 539

Query 541  NCERYNSQVCGGSDRGSCNCGKCSCKPGYEGSACQCQRSTTGCLNARLVECSGRGHCQCN 600
          NCERYN QVCGG RG C CGKC C PG+EGSACQC+R+T GCLN R VECSGRG C+CN
Sbjct 540  NCERYNQVCGGPGRGLCFCKCRCHPGFEGSACQCERTTEGCLNPRRVECSGRGRCRCN 599

Query 601  RCICDEGYQPPMCEDPCSGSHCRDNHTSCAECLKFKDKGPFKNCQSVQCAGMTLQTIPLK 660
          C C GYQ P+C++CP C S C + SCAECLKF+KGPF KNCS C G+ L P+K
Sbjct 600  VCECHSGYQLPLCQECPGCPSPC-GKYISCAECLKFEKGPFGKNCSAACPGQLSNNPVK 658
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Query 661 KKPCKERDSEGCWITYTLQQKDGRNIYNIHVEDSLECVKGPNVAAivggtvvvgvligvl 720  
+ CKERDSEGCW+ YTL+Q+DG + Y I+V++S ECV GPN+AAIVGGTV G+VLIG+L  
Sbjct 659 GRTCKERDSEGCWVAYTLEQQDGMDRYLIYVDESRECVAGPNIAAIVGGTVAGIVLIGIL 718

Query 721 llviWKALHTLDLREYRRFEKEKLKSQWNNNDNPLFKSATTVMNPKFAES 771  
LLVIWKAL HL+DLREYRRFEKEKLKSQWNNNDNPLFKSATTVMNPKFAES  
Sbjct 719 LLVIWKALIHLSDLREYRRFEKEKLKSQWNNNDNPLFKSATTVMNPKFAES 769

CD23: 54%

>ref|NP\_001993.2| Fc fragment of IgE, low affinity II, receptor for (CD23A) [Homo sapiens]  
Length=321

GENE ID: 2208 FCER2 | Fc fragment of IgE, low affinity II, receptor for (CD23)  
[Homo sapiens] (Over 10 PubMed links)

Score = 373 bits (957), Expect = 1e-103

Identities = 179/331 (54%), Positives = 236/331 (71%), Gaps = 23/331 (6%)

```
Query 1  MEENEYSGYWEPKRKRCCARRGTQLMLVGLLSTAMWAG11a1111WHWETEKNLKQLGD 60
      MEE +YS  E PR+RCC  RRGTQ++L+GL++ A+WAGLL LLLLWHW+T ++LKQL +
Sbjct 1  MEEGQYSEIEELPRRCC--RRGTQIVLLGLVTAALWAGLLTLLLLWHWDTTQSLKQLEE 58

Query 61  TAIQNVSHVTKDLQKFQSNQLAQKSQVQMSQNLQELQAEQKQMKQAQDSRLSQNLTLGLQE 120
      A +NVS V+K+L+  +Q+AQKSQ  Q+SQ L+EL+AEQ+++K+QD  LS NL G
Sbjct 59  RAARNVSQVSKNLESHHGDQMAQKSQSTQISQELEELRAEQRLKSQDLELSWNLG--- 115

Query 121  DLRNAQSQNSKLSQNLNRLQDDLVDNIKSLGLNEKRTASDSLEKLQEEVAKLWIEILISKG 180
      LQ DL + KS  LNE+  ASD LE+L+EEV KL +E+ +S G
Sbjct 116  -----LQADLSSFKSQELNERNEASDLLERLREEVTKLRMELQVSSG 157

Query 181  TACNICPKNLWHFQKCYFYGKSGKQWIQARFACSDLQGRVLSIHSQKEQDFLMQHINKK 240
      CN CP+ W++FQ+KCYFYGKG+KQW+ AR+AC D++G+LVSIS +EQDFL +H +
Sbjct 158  FVCNTCPEKWINFQRKCYFYGKGTKQVWHARYACDDMEGQLVSIHSPEEQDFLTKHASHT 217

Query 241  DSWIGLQDLNMEGEFVWSDGSPVGYSnwnpgepnnggqgeDCVMMRGSGQWDAFCRSYL 300
      SWIGL++L+++GEF+W DGS V YSNW PGEP + QGEDCVMMRGSG+WDAFC  L
Sbjct 218  GSWIGLRNLDLKGEFIWVDGSHVDYSNWAPGEPTSRSQGEDCVMMRGSGRWDAFCDRKL 277

Query 301  DAWVCEQLATCEISAPLASVTPTPTPKSEP 331
      AWVC++LATC  A  S  P  + +P
Sbjct 278  GAWVCDRLATCTPPASEGSAESMGPDSPDP 308
```

ICAM-1: 53%

>ref|NP\_000192.1| intercellular adhesion molecule 1 precursor [Homo sapiens]  
Length=532

GENE ID: 3383 ICAM1 | intercellular adhesion molecule 1 (CD54), human  
rhinovirus receptor [Homo sapiens] (Over 100 PubMed links)

Score = 525 bits (1352), Expect = 4e-149

Identities = 287/540 (53%), Positives = 363/540 (67%), Gaps = 11/540 (2%)

```
Query 1  MASTRAKptlplllalvtvvIPGPGDAQVSIHPREAFLPQGGSVQVNCSSSCKEDLSLGL 60
      MA + +P LP LL L+ + PGP+AQ S+ P + LP+GGSV V CS+SC + LG+
Sbjct 1  MAPSSPRPALPALLVLLGALFPGPGNAQTSVSPSKVILPRGGSVLVTCSTSCDQPKLLGI 60

Query 61  ETQWLKDELE-SGPNWKLFESEIGEDSSPLCFENC GTVQSSASATITVVSFPESVELRP 119
      ET K EL G N K++ELS + EDS P+C+ NC QS+A +TVY PE VEL P
Sbjct 61  ETPLPKKELLPLGNRKVVELSNVQEDSQPMCSNCPDQGSTAKTFLTIVYWTPERVELAP 120

Query 120  LPAWQQVGKDLTLRCHVDGGAPRTQLSAVLLRGEEILSRQPVGGHPKDPKEITFTVLASR 179
      LP+WQ VGK+LTLRC V+GGAPR L+ VLLRGE+ L R+P G +P E+T TVL R
Sbjct 121  LPSWQPVGKNLTLRCQVEGGAPRANLTVVLLRGEKELKREPAVG---EPAEVTTTVLVR 177

Query 180  GDHGANFSCRTDLRLPQGLALFSNVSEARSLRTFDLPATIPKLDTPDLLEVGTQQKLC 239
      HGANFSCRTDLRLPQGL LF N S L+TF LPAT P+L +P +LEV TQ + C
Sbjct 178  DHGANFSCRTDLRLPQGLELFENTSAPYQLQTFVLPATPPQLVSPRVLEVDTQGTVC 237

Query 240  SLEGLFPASEARIYLELGGQMPTQESTNSSDSVSATALVEVTEEFDRTLPLRCVLELADQ 299
      SL+GLFP SEA+++L LG Q T +DS SA A V VT E + T L C + L +Q
Sbjct 238  SLDGLFPVSEAQVHLALGDQRLNPTVTYGNDSFSAKASVSVTADEGTQRLTCAVILGNQ 297

Query 300  ILETQRTLTVYNFSAPVLTLSQLEVSEGSQVTVKCEAHSGSKVLLSGVEPRPPTPQVQF 359
      ET +T+T+Y+F AP + L++ EVSEG++VTVKCEAH +KV L+GV +P P+ Q
Sbjct 298  SQETLQTVTIYSFPAPNVILTKPEVSEGTEVTVKCEAHPRAKVT-LNGVPAQLGPRAQL 356

Query 360  TLNASEDHKRSFFCSAALEVAGKFLFKNQTLHLVLYGPRLDETDCLGNTWQEGSQQT 419
      L A+ ED+ RSF CSA LEVAG+ + KNQT EL VLYGPRLDE DC GNWTW E SQQT
Sbjct 357  LLKATPEDNGRSFSCSATLEVAGQLIHKNTRELRLVLYGPRLDERDCPGNWTWPENSQQT 416

Query 420  LKCQAWGNPSPKMTCCRKADGAL-LPIGVVKSVMQEMNGTYVCHAFSSHGNVTRNVYLT 478
      CQAWGNP P++ C + DG LPIG +V +++ GTY+C A S+ G VTR V + V
Sbjct 417  PMCQAWGNPLPELKCLK--DGTFLPIGESVTVTRDLEGTYLCCRARSTQGEVTRETVNV 474

Query 479  LYHSQNNWTiilvpvllvivglvMAASYVYNRQRKIRIYKLQKAQE-EAIKLKGQAPPP 537
      L S +II V VI+G ++Y+YNRQRKI+ Y+LQ+AQ+ +K QA PP
Sbjct 475  L--SPRYEIVIIITVAAAVIMGTAGLSTYLYNRQRKIKKYRLQQAQKGTMPKPNTQATPP 532
```

VLA-4 Integrin Receptor: 84%

>ref|NP\_000876.3| integrin alpha 4 precursor [Homo sapiens]

Length=1032

GENE ID: 3676 ITGA4 | integrin, alpha 4 (antigen CD49D, alpha 4 subunit of VLA-4 receptor) [Homo sapiens] (Over 10 PubMed links)

Score = 1790 bits (4636), Expect = 0.0

Identities = 871/1025 (84%), Positives = 951/1025 (92%), Gaps = 0/1025 (0%)

Query	15	DQGPRGIALREAVMLLLYFGVPTGPSYNLDPENALLYQGPGSTLFGYSVVLHSHGSKRWL	74
		+ GPR A+RE VMLLL GVPTG YN+D E+ALLYQGP TLFGYSVVLHSHG+ RWL	
Sbjct	8	EPGPRRAAVRETVMLLCLGVPTGRPYNVDTESALLYQGPHTLFGYSVVLHSHGANRWL	67
Query	75	IVGAPTASWLSNASVVPNGAIYRCGIRKNPNQTCEQLQSGSPSGEPCGKTCLEERDNQWL	134
		+VGAPTA+WL+NASV+NGPAIYRC I KNP QTCEQLQ GSP+GEPGKTCLEERDNQWL	
Sbjct	68	LVGAPTANWLANASVINPGAIRIGKNPGQTCEQLQLGSPNGEPCGKTCLEERDNQWL	127
Query	135	GVTLSRQPGENGSIIVTCGHRWKNIFYMKSDNKLPTGICYVMPSDLRTELSKRMAPCYKDY	194
		GVTLSRQPGENGSIIVTCGHRWKNIFY+K++NKLPTG CY +P DLRTLSKR+APCY+DY	
Sbjct	128	GVTLSRQPGENGSIIVTCGHRWKNIFYIKNENKLPTGGCYGVPPDLRTELSKRIAPCYQDY	187
Query	195	TRKGFENFASCQAGISSFYTDLIVMGAPGSSYWTGTVFVYNITTNQYKAFVDRQNQVKF	254
		+KGFENFASCQAGISSFYT+DLIVMGAPGSSYWTG++FVYNITTN+YKAF+D+QNQVKF	
Sbjct	188	VKKGFENFASCQAGISSFYTKDLIVMGAPGSSYWTGSLFVYNITTNKYKAFLDKQNQVKF	247
Query	255	GSYLGYSVGAGHFRSPHTTEVVGGAPQHEQIGKAYIFSIDENELNIVYEMKGKLGSYFG	314
		GSYLGYSVGAGHFRS HTTEVVGGAPQHEQIGKAYIFSIDE ELNI++EMKGKLGSYFG	
Sbjct	248	GSYLGYSVGAGHFRSQHTTEVVGGAPQHEQIGKAYIFSIDEKELNILEMKGKLGSYFG	307
Query	315	ASVCAVDLNADGFSDDL VGAPMQSTIREEGRVFVYINSGMGAVMVEMERVLVGS DKYAAR	374
		ASVCAVDLNADGFSDDL VGAPMQSTIREEGRVFVYINSG GAVM ME LVGS DKYAAR	
Sbjct	308	ASVCAVDLNADGFSDDL VGAPMQSTIREEGRVFVYINSGGAVMNAMETNLVGS DKYAAR	367
Query	375	FGESIANLGDIDNDGFEDIAIGAPQEDDLRGAVYIYNGRVDGISSTYSQRIEQQISKSL	434
		FGESI NLGDIDNDGFED+AI GAPQEDDL+GA+YIYNGR DGISST+SQRIEQ QISKSL	
Sbjct	368	FGESIVNLGDIDNDGFEDVAIGAPQEDDLQGAIIYNGRADGISSTFSQRIEGLQISKSL	427
Query	435	RMFGQSIGQIDADNNGYVDVAVGAFQSDSAVLLRTRPVVIVEASLSHPESVNR TKFDC	494
		MFGQSIGQIDADNNGYVDVAVGAF+SDSAVLLRTRPVVIV+ASLSHPESVNR TKFDC	
Sbjct	428	SMFGQSIGQIDADNNGYVDVAVGAFRSDSAVLLRTRPVVIVDASLSHPESVNR TKFDCV	487
Query	495	ENGLPSVCMHLTLCF SYKGKEVPGYIVLFYNVSLDVHRKAESPSRFYFFSNGTSDVITGS	554
		ENG PSVC+ LTLCF SYKGKEVPGYIVLFYN+SLDV+RKAESP RFYF SNGTSDVITGS	
Sbjct	488	ENGWPSVCIDLTLCF SYKGKEVPGYIVLFYNMSLDVNRKAESP RPFRYFSSNGTSDVITGS	547
Query	555	IRVSSSGEKRTHQAFMRKDVRDILTPIHVEATYHLGHHVITKRNTTEFPPLQPI LQKK	614
		I+VSS CRTHQAFMRKDVRDILTPI +EA YHLG HVI+KR+TEFPPLQPI LQKK	
Sbjct	548	IQVSSREANCRTHQAFMRKDVRDILTPIQIEAAYHLGPHVISKRSTEEFPPLQPI LQKK	607
Query	615	EKDVIKRMINFARFCAYENCSADLQVSAKVGFLKPYENKTYLAVGSMKTM LNVS LFNAG	674
		EKD+++K INFARFCA+ENCSADLQVSAK+GFLKP+ENKTYLAVGSMKT+MLNVS LFNAG	
Sbjct	608	EKDIMKKTINFARFCAHENSADLQVSAKIGFLKPHENKTYLAVGSMKTM LNVS LFNAG	667

Query	675	DDAYETTLNVQLPTGLYFIKILDLEEKQINCEVTESSGIVKLACSLGYIYVDRLSRIDIS	734
		DDAYETTL+V+LP GLYFIKIL+LEEKQINCEVT++SG+V+L CS+GYIYVD LSRIDIS	
Sbjct	668	DDAYETTLHVKLPVGLYFIKILELEEKQINCEVTDN SGVVQLDCSIGIYVDHLSRIDIS	727
Query	735	FLLDVSSLSRAHEDLSISVHASCENEGELDQVRDNRVTLTIPLRYEVM LTVHGLVNPTSF	794
		FLLDVSSLSRA EDLSI+VHA+CENE E+D ++ +RVT+ IPL+YEV LTVHG VNPTSF	
Sbjct	728	FLLDVSSLSRAEEDLSITVHATCENEEEMDNLKHSRVTVAIPLKYE VKLTVHGFVNPTSF	787
Query	795	VYGSSEENEPETCMAEKLNLTFHVINTGISMAPNVSVKIMVPNSFLPQDDKLFNVLDVQT	854
		VYGS++ENEPETCM EK+NLTFHVINTG SMAPNVSV+IMVPNSF PQ DKLFN+LDVQT	
Sbjct	788	VYGSNDENEPETCMVEKMNLTFHVINTGNSMAPNVSV+IMVPNSFSPQTDKLFNILDVQT	847
Query	855	TTGQCHFHKHYGRECTFAQQKGIAGTLTDIVKFLSKTDKRLLYCMKADQHCLDFLCNFGKM	914
		TTG+CHF++Y R C QQK TL IV+FLSKTDKRLLYC+KAD HCL+FLCNFGKM	
Sbjct	848	TTGECHFENYQRVCALEQQKSAMQTLKGIVRFLSKTDKRLLYCIKADPHCLNFCNFGKM	907
Query	915	ESGKEASVHIQLEGRPSILEMDETSSLKFEIKATAFPEPHPKVIELNKDENVAHV FLEGL	974
		ESGKEASVHIQLEGRPSILEMDETS+LKFEI+AT FPEP+P+VIELNKDENVAHV LEGL	
Sbjct	908	ESGKEASVHIQLEGRPSILEMDETSALKFEIRATGFPEPNRVIELNKDENVAHV LLEGL	967
Query	975	HHQRPKRHFTiiiiitislllglivllliSCVMWKAGFFKRQYKSILQEENRRDSWSYVNS	1034
		HHQRPKR+FTI+II+ SLLGLIVLLIS VMWKAGFFKRQYKSILQEENRRDSWSY+NS	
Sbjct	968	HHQRPKRVFTIVIISSSLLGLIVLLISYVMWKAGFFKRQYKSILQEENRRDSWSYINS	1027
Query	1035	KSND	1039
		KSND	
Sbjct	1028	KSND	1032

IL-1 $\beta$  Receptor: 62%

>ref|NP\_004624.1| interleukin 1 receptor, type II precursor [Homo sapiens]  
ref|NP\_775465.1| interleukin 1 receptor, type II precursor [Homo sapiens]  
Length=398

GENE ID: 7850 IL1R2 | interleukin 1 receptor, type II [Homo sapiens]  
(Over 10 PubMed links)

Score = 474 bits (1220), Expect = 5e-134  
Identities = 231/371 (62%), Positives = 280/371 (75%), Gaps = 2/371 (0%)

```
Query 28  NCQFRGREFKSELRLGEGPVVLRCLAPhsdisssshsF-LTWSKLDSSQLIP-RDEPRM 85
          +C+FRGR +K E RLEGE PV LRCP P+ +S S LTW K DS++ +P +E RM
Sbjct 27  SCRFRGRHYKREFRLEGE PVALRCPQVPYWLWASVSPRINLTWHKNSARTVPGEETR M 86

Query 86  WVKGNI LWILPAVQQDSGT YICTFRNASHCEQMSVELKVFNTEASLPHVSYLQISALST 145
          W + LW+LPA+Q+DSGT Y+CT RNAS+C++MS+EL+VF+NT+A LP +SY QI LST
Sbjct 87  WAQD GALWLLPALQEDSGTYVCTTRNASYCDKMSIELRVFENTDAFLPFISYPQILTST 146

Query 146 TGLLVCPDLKEFISSNADGKI QWYKGAILLDKGNKEFLSAGDPTRLISNTSMDDAGYYR 205
          +G+LVCPDL EF D KI QWYK ++LLDK N++FLS T LL+ + +++DAGYYR
Sbjct 147 SGVLVCPDLSEFTRDKTDVKIQWYKDSLLLDKDNKEFLSVRGTTLLVHDVALEDAGYYR 206

Query 206 CVMFTFYNGQEYNITRNI ELRVKGTTEPIPVIIISPLETIPASLG SRLIVPCKVFLGTGT 265
          CV+TF + GQ+YNITR+IELR+K E IPVIIISPL+TI ASLG SRL +PCKVFLGTGT
Sbjct 207 CVLTF AHEGQQYNITRSIELRIKKKKEETIPVIIISPLKTISASLG SRLTIPCKVFLGTGT 266

Query 266 SSNTIVWWLANSTFISAAYPRGRVTEGLHHQYSEN DENYEVSLIFDPVTREDLHTDFKC 325
          T++WW AN T I +AYP GRVTEG +YSEN+ENY+EV LIFDPVTREDLH DFKC
Sbjct 267 PLTTMLWWTANDTHIESAYPGGRVTEGPRQEYSENNENYIEVPLIFDPVTREDLHMDFKC 326

Query 326 VASNPRSSQSLHTTVKEVSSTFSW sialaplsliilVVGAIWMRRRCKRRAGKTYGLTKL 385
          V N S Q+L TTVKE SSTFSW I LAPLSL LV+G IWM RRCK R GK GLT L
Sbjct 327 VVHNTLSFQTLRTTVKEASSTFSWGIVLAPLSLAFLVLGGIWMHRRCKHRTGKADGLTVL 386

Query 386 RTDNQDFPSSP 396
          +QDF S P
Sbjct 387 WPHHQDFQSY P 397
```



GPIIb: 79%

>ref|NP\_000410.2| integrin alpha 2b preproprotein [Homo sapiens]  
Length=1039

GENE ID: 3674 ITGA2B | integrin, alpha 2b (platelet glycoprotein IIb of IIb/IIIa complex, antigen CD41) [Homo sapiens] (Over 100 PubMed links)

Score = 1681 bits (4354), Expect = 0.0

Identities = 831/1040 (79%), Positives = 910/1040 (87%), Gaps = 11/1040 (1%)

Query	1	MARASCAWHSLWLLQWTPFLGPSAVPPVWALNLDSEKFSVYAGPNGSHFGFSVDFHKDK	60
		MARA C +LWLL+W L LCP A PP WALNLD + + YAGPNGS FGFS+DFHKD	
Sbjct	1	MARALCPLQALWLEWVLLLLGPCAAPWALNLDPVQLTFYAGPNGSQFGFSLDFHKDS	60
Query	61	HGSVSIVVGAPRALNASQEETGAVFLCPWKANGGKCNPLLFDLRDETRNLGFQIFQTFTKT	120
		HG V+IVVGAPR L SQEETG VFLCPW+A GG+C LFLDLRDETRN+G Q QTFK	
Sbjct	61	HGRVAIVVGAPRTLGPSQEETGGVFLCPWRAEGGQCPSSLFLDLRDETRNVGSQTLQTFKA	120
Query	121	GQGLGASVVSNDVIVACAPWQHWNVLEKRDEAEKTPVGGCFLAQLQSGGRAEYSPCRAN	180
		QGLGASVVS+W+DVIVACAPWQHWNVLEK +EAEKTPVG CFLAQ +SG RAEYSPCR N	
Sbjct	121	RQGLGASVVSNDVIVACAPWQHWNVLEKTEEAETPVGSCFLAQPESGRRAEYSPCRGN	180
Query	181	TMSSVYAES-FRGDKRYCEAGFSLAVTQAGELVLGAPGGYFFLGLLARVPIENIISTYRP	239
		T+S +Y E+ F DKRYCEAGFS VTQAGELVLGAPGGY+FLGLLA+ P+ +I S+YRP	
Sbjct	181	TLSRIYVENDFSWDKRYCEAGFSSVVTQAGELVLGAPGGYFFLGLLAQAPVADIFSSYRP	240
Query	240	GTLWHVSNQRFTYDNSNPVFFDGYRGYSVSVGEFDGDPSTTEYVSGAPTWSWTLGAVEI	299
		G LLWHVS+Q ++D+SNP +FDGY GYSV+VGEFDGD +TTEYV GAPTWSWTLGAVEI	
Sbjct	241	GILLWHVSSQSLSFDSNPYFDGYWGYSAVGEFDGDLNTEYVVGAPTWSWTLGAVEI	300
Query	300	LDSYYQLHRLHGEQMASYFGHSVAVTDVNGDGRHDLLVGAPLYMESRADRKLAEVGRVY	359
		LDSYYQ LHLR GEQMASYFGHSVAVTDVNGDGRHDLLVGAPLYMESRADRKLAEVGRVY	
Sbjct	301	LDSYYQLHRLRGEQMASYFGHSVAVTDVNGDGRHDLLVGAPLYMESRADRKLAEVGRVY	360
Query	360	LFLQPKGPQALSTPTLLLTGTQLYGRFGSAIAPLGDLNRDGYNDIAVAAPYGGPSGQGQV	419
		LFLQP+GP AL P+LLLTGTQLYGRFGSAIAPLGDL+RDGYNDIAVAAPYGGPSG+GQV	
Sbjct	361	LFLQPRGPHALGAPSLLLTGTQLYGRFGSAIAPLGDLDRDGYNDIAVAAPYGGPSGRGQV	420
Query	420	LIFLGQSEGLSPRPSQVLDSPFPTGSGFGFSLRGAVDIDDNGYPDLIVGAYWASKVAVYR	479
		L+FLGQSEGL RPSQVLDSPFPTGS FGFSLRGAVDIDDNGYPDLIVGAY A++VAVYR	
Sbjct	421	LVFLGQSEGLSRPSQVLDSPFPTGSFSGFSLRGAVDIDDNGYPDLIVGAYGANQVAVYR	480
Query	480	AQPGVMATVQLMVQDSLNP TLKNCVLDQTKTPVSCFNIQMCVGATGHNIPQKLHLKAEQ	539
		AQP V A+VQL+VQDSLNP +K+CVL QTKTPVSCFNIQMCVGATGHNIPQKL L AELQ	
Sbjct	481	AQPVVKASVQLLVQDSLNPVAVKSCVLPQTKTPVSCFNIQMCVGATGHNIPQKLSLNAELQ	540
Query	540	LDLQKPRQRRVlllasqqasltlsldIGGRDKPICHHTGAFLRDEADFRDKLSPIVLSL	599
		LD QKPRQRRVLLL SQA TL+LDLGG+ PICHHT AFLRDEADFRDKLSPIVLSL	
Sbjct	541	LDRQKPRQRRVLLLSQAAGTTLNLDLGGKHSPICHHTMAFLRDEADFRDKLSPIVLSL	600
Query	600	NVSLPPEETGGAPAVVLHGETHVQEQTRIILDCGEDDLCPQLRLTATAGDSPLLIGADN	659
		NVSLPP E G APAVVLHG+THVQEQTRI+LDCGEDD+CVPL+LTA+ SPL+GADN	
Sbjct	601	NVSLPTEAGMAPAVVLHGDTHVQEQTRIVLDCGEDDVCVPLQLTASVTGSPLLVGADN	660

Query	660	VLELKIEAANDGEGAYEAELAVHLP GAHYMRALSNI EGFERLVCTQKKENESRVALCEL	719
		VLEL+++AAN+GEGAYEAELAVHLP GAHYMRALSNI+EGFERL+C QKKENE+RV LCEL	
Sbjct	661	VLELQMDAANE GEGAYEAELAVHLPQGAHYMRALSNI+EGFERLICNQKKENETRVLCEL	720
Query	720	GNPMKKDTRIGITMLVSVENLEEAGESVSFQLQVRSKNSQNPNSKVMLPVAIQAEATVE	779
		GNPMKK+ +IGI MLVSV NLEEAGESVSFQLQ+RSKNSQNPNSK+V+L V ++AEA VE	
Sbjct	721	GNPMKKNAGIAMIAMLVSVGNLEEAGESVSFQLQIRSKNSQNPNSKIVLLDVPVRAEAQVE	780
Query	780	LRGNSFPASLVVAAEEGDREQEDLDSWVSRL EHTYELHNIGPCTVNGLRLLIHIPGQSQP	839
		LRGNSFPASLVVAAEEG+REQ LDSW ++EHTYELHN GPCTVNGL L IH+PGQSQP	
Sbjct	781	LRGNSFPASLVVAAEEGEREQNSLDSWGPKEHTYELHNNGPCTVNGLHLSIHLPGQSQP	840
Query	840	SDLLYILDVQPQGGLLCSTQPSP---KVDWKLSTPSPSSIRPVHHQRERRQAFLQGPKPG	896
		SDLLYILD+QPQGGL C QP KVDW L PPS I P HH+R+RRQ FL P+P	
Sbjct	841	SDLLYILDIQPQGGLQCFPPVPVNLKVDWGLPIPSPIHPAHHKDRRQIFL--PEPE	898
Query	897	Q---QDPVLVSCDGSASCTVVECELREMV RGQAMVTVMQAMGLSSLRQRPQE QFVLQS	952
		Q QDPVLVSCD SA CTVV+C+L+EM RGQAMVTV A L L SL QRP +QFVLQS	
Sbjct	899	QPSRLQDPVLVSCD-SAPCTVVQCDLQEMARGQAMVTVLAFLWLP SLYQRPLDQFVLQS	957
Query	953	HAWFNvsslpsvpsvslpsGQARVQTQLLRALEERAIPVWVlvglgglllltllvIA	1012
		HAWFNVSSLPY+VP +SLP G+A+V TQLLRALEERAIP+WWVLGVLGGLLLLT+LVLA	
Sbjct	958	HAWFNVSSLPYAVPPLSLPRGEAQVWTQLLRALEERAIPVWVLGVLGGLLLLTILVLA	1017
Query	1013	MWKAGFFKRNRPPEEDEEE	1032
		MWK GFFKRNRPPEED+EE	
Sbjct	1018	MWKGFFKRNRPPEEDDEE	1037

GPIIb Receptor: 90%

>ref|NP\_000203.2| integrin beta chain, beta 3 precursor [Homo sapiens]  
Length=788

GENE ID: 3690 ITGB3 | integrin, beta 3 (platelet glycoprotein IIb, antigen CD61) [Homo sapiens] (Over 100 PubMed links)

Score = 1513 bits (3918), Expect = 0.0

Identities = 711/782 (90%), Positives = 751/782 (96%), Gaps = 0/782 (0%)

Query	6	PGQLWaalalgalagvvvgESNICTRGVNSCQCLAVSPVCAWCSDETL	SQSPRCNL	65
		P LWA +LALGALAGV VG NICTTRGV+SCQCLAVSP+CAWCSDE L	GSPPRC+L	
Sbjct	7	PRPLWATVLALGALAGVGVPNICTRGVSSCQCLAVSPMCAWCSDEALPLGSPRCDL		66
Query	66	KENLLKDNCAPIESIEFPVSEAQILEARPLSSKSGSSAQITQVSPQRIALRLRPDDSKIF		125
		KENLLKDNCAPIESIEFPVSEA++LE RPLS KSGS S+Q+TQVSPQRIALRLRPDDSK F		
Sbjct	67	KENLLKDNCAPIESIEFPVSEARVLEDRPLSDKSGSDSSQVTQVSPQRIALRLRPDDSKNF		126
Query	126	SLQVRQVEDYPVDIYYLMDLSFSMKDDLSSIQTGLTKLASQMRKLTSLRIGFGAFVDKP		185
		S+QVRQVEDYPVDIYYLMDLS+SMKDDL SIQ LGTKLA+QMRKLTSLRIGFGAFVDKP		
Sbjct	127	SIQVRQVEDYPVDIYYLMDLSYSMKDDLWSIQNLGTLKATQMRKLTSLRIGFGAFVDKP		186
Query	186	VSPYMYISPPQAIKNPCYNMKNACLPMFGYKHVLTLDQVSRFNEEVKKQSVSRNRDAPE		245
		VSPYMYISPP+A++NPCY+MK CLPMFGYKHVLTLDQV+RFNEEVKKQSVSRNRDAPE		
Sbjct	187	VSPYMYISPPALENPCYDMKTTCLPMFGYKHVLTLDQVTRFNEEVKKQSVSRNRDAPE		246
Query	246	GGFDAIMQATVCDEKIGWRNDASHLLVFTTDAKTHIALDGRLAGIVLPNDGHCHIGTDNH		305
		GGFDAIMQATVCDEKIGWRNDASHLLVFTTDAKTHIALDGRLAGIV PNDG CH+G+DNH		
Sbjct	247	GGFDAIMQATVCDEKIGWRNDASHLLVFTTDAKTHIALDGRLAGIVPNDGQCHVGSDNH		306
Query	306	YSASTTMDYPSLGLMTEKLSQKNINLIFAVTENVVSLYQNYSELIPGTTVGVLSDSSNV		365
		YSASTTMDYPSLGLMTEKLSQKNINLIFAVTENVV+LYQNYSELIPGTTVGVLSDSSNV		
Sbjct	307	YSASTTMDYPSLGLMTEKLSQKNINLIFAVTENVVNLQNYSELIPGTTVGVLSDSSNV		366
Query	366	LQLIVDAYGKIRSKVELEVRDLPEELSLSFNATCLNNEVIPGLKSCVGLKIGDVSFSIE		425
		LQLIVDAYGKIRSKVELEVRDLPEELSLSFNATCLNNEVIPGLKSC+GLKIGDVSFSIE		
Sbjct	367	LQLIVDAYGKIRSKVELEVRDLPEELSLSFNATCLNNEVIPGLKSCMGLKIGDVSFSIE		426
Query	426	AKVRGCPQEKEQSFTIKPVGFKDSLTVQVTFDCDCACQAFAPSSPRCNGNGTFECGVC		485
		AKVRGCPQEKE+SFTIKPVGFKDSL VQVTFDCDCACQA A+P+S RCNNGNGTFECGVC		
Sbjct	427	AKVRGCPQEKEQSFTIKPVGFKDSLIVQVTFDCDCACQAQAPNSHRCNNGNGTFECGVC		486
Query	486	RCDQGWLGSMCESEEDYRPSQQEECSPEKQPICSQRGECLCGQCVCHSSDFGKITGKY		545
		RC GWLGS CECSEEDYRPSQQ+ECSP+EGQP+CSQRGECLCGQCVCHSSDFGKITGKY		
Sbjct	487	RCGPWLGSGCESEEDYRPSQQDECSPEKQPVCSQRGECLCGQCVCHSSDFGKITGKY		546
Query	546	CECDDFSCVRYKGEMCSGHGQCNCDCVCDSDWTGYCNCCTTRTDCMSTNGLLCSGRGN		605
		CECDDFSCVRYKGEMCSGHGQC+CGDC+CDSDWTGYCNCCTTRTDCMS+NGLLCSGRG		
Sbjct	547	CECDDFSCVRYKGEMCSGHGQCSCGDCDCSDWTGYCNCCTTRTDCMSSNGLLCSGRGK		606
Query	606	CECGSCVCVQPGSYGDTCEKCPCTPDACSFKKECVECKKFNRGTLHEENTCSRYCRDDIE		665
		CECGSCVC+QPGSYGDTCEKCPCTPDAC+FKKECVECKKF+RG LH+ENTC+RYCRD+IE		
Sbjct	607	CECGSCVCIQPGSYGDTCEKCPCTPDACFVKKECVECKKFDRGALHDENTCNRYCRDEIE		666

Query	666	QVKELDTGKNAVNTYKNEDDCVVRFQYYEDTSGRAVLVVEEPEC PKGPDILVVLLSV	725
		VKEL DTGK+AVNCTYKNEDDCVVRFQYYED+SG+++LYVVEEPEC PKGPDILVVLLSV	
Sbjct	667	SVKELKDTGKDAVNCTYKNEDDCVVRFQYYEDSSGKSILYVVEEPEC PKGPDILVVLLSV	726
Query	726	MgailliglatlliwkllitiHDrkefakfeerarakWDANNPLYKEATSTFTNITYR	785
		MGAILLIGLA LLIWKLLITIHDRKEFAKFEERARAKWDANNPLYKEATSTFTNITYR	
Sbjct	727	MGAILLIGLAALLIWKLLITIHDRKEFAKFEERARAKWDANNPLYKEATSTFTNITYR	786
Query	786	GT	787
		GT	
Sbjct	787	GT	788

PAI-1: 78%

>ref|NP\_000593.1| plasminogen activator inhibitor-1 [Homo sapiens]  
Length=402

GENE ID: 5054 SERPINE1 | serpin peptidase inhibitor, clade E (nexin,  
plasminogen activator inhibitor type 1), member 1 [Homo sapiens]  
(Over 100 PubMed links)

Score = 630 bits (1626), Expect = 0.0  
Identities = 316/402 (78%), Positives = 357/402 (88%), Gaps = 0/402 (0%)

```
Query 1  MQMSSALACLILGLVLVSGKGFTLPLRESHTAHQATDFGKVFQQVQASKDRNVVFSKY 60
        MQMS AL CL+LGL LV G+G + S+ AH A+DFGV+VFQQV QASKDRNVVFSKY
Sbjct 1  MQMSPALTCLVLGLALVFGEGSAVHPPSYVAHLASDFGVRVFQQVAQASKDRNVVFSKY 60

Query 61 GVSSVLAMLQMTTAGKTRRQIQDAMGFKVNEKGTAHALRQLSKELMGPWNKNEISTADAI 120
        GV+SVLAMLQ+TT G+T++QIQ AMGFK+++KG A ALR L KELMGPWNK+EIST DAI
Sbjct 61 GVASVLAMLQLTTGGETQQQIQAAAMGFKIDDKGMAPALRHLYKELMGPWNKDEISTDAI 120

Query 121 FVQRDLVLVQGFMPHFFKLFQTMVKQVDFSEVERARFIINDWVERHTKGMINDLLAKGAV 180
        FVQRDL+LVQGFMPHFF+LF++ VKQVDFSEVERARFIINDWV+ HTKGM++LL KGAV
Sbjct 121 FVQRDLKLVLQGFMPHFFRLFRSTVKQVDFSEVERARFIINDWVKTHTKGMISNLLKGAV 180

Query 181 DELTRLVLVNALYFSGQWKTPFLEASTHQRLFHKS DGSTVSPMMAQSNKFNYTEFTTPD 240
        D+LTRLVLVNALYF+GQWKTPF ++STH+RLFHKS DGSTVSPMMAQ+NKFNYTEFTTPD
Sbjct 181 DQLTRLVLVNALYFNGQWKTPFPDSSTHRRLLFHKS DGSTVSPMMAQTNKFNYTEFTTPD 240

Query 241 GLEYDVVELPYQRDTLSMFIAAPFEKDVHLSALTNILDAELIRQWKGNMTRLPRLLILPK 300
        G YD++ELPY DTLSMFIAAP+EK+V LSALTNIL A+LI WKGNMTRLPRLL+LPK
Sbjct 241 GHYYDILELPYHGDTLSMFIAAPYEKEVPLSALTNILSAQLISHWKGNMTRLPRLLVLPK 300

Query 301 FSLETEVDLRGPLEKLGMPDMFSATLADFTSLSDQEQLSVAQALQKVRIEVNESGTVASS 360
        FSLETEVDLR PLE LGM DMF ADFTSLSDQE L VAQALQKV+IEVNESGTVASS
Sbjct 301 FSLETEVDLRKPLENLGMTDMFRQFQADFTSLSDQEPLHVAQALQKVRIEVNESGTVASS 360

Query 361 STAFVISARMAPTEMVIDRSFLFVVRHNPTETILFMGQVMEP 402
        STA ++SARMAP E+++DR FLFVVRHNPT T+LFMGQVMEP
Sbjct 361 STAVIVSARMAPEEIIMDRPFLFVVRHNPTGTVLFMGQVMEP 402
```

IL-4 Receptor: 52%

>emb|CAD12326.1| unnamed protein product [Homo sapiens]  
emb|CAD28170.1| unnamed protein product [Homo sapiens]  
emb|CAD28391.1| unnamed protein product [Homo sapiens]  
emb|CAJ01243.1| unnamed protein product [Homo sapiens]  
Length=825

Score = 799 bits (2064), Expect = 0.0

Identities = 427/816 (52%), Positives = 519/816 (63%), Gaps = 21/816 (2%)

```
Query 1  MGR LCTKFLTSVGCLILLVLTGSGSIKVLGEPTCFSDYIRTSTCEWFLDSAVDCSSQLCL 60
          MG LC+ L V CL+LL V SG++KVL EPTC SDY+ STCEW ++ +CS++L L
Sbjct 1  MGWLCSGLLFPVSVCLVLLQVASSGNMKVLQEPTCVSDYMSISTCEWKMGPTNCSTELRL 60

Query 61  HYRLMFFEFSENLTICIPNSASTVCVCHMEMNRPVQSDRYQMELWAEHRQLWQGSFSPSG 120
          Y+L+F SE TCIP N+ CVCH+ M+ V +D Y ++LWA + LW+GSF PS
Sbjct 61  LYQLVFL-LSEAHTCIPENNGGAGCVCHLLMDDVVSADNYTLDLWAGQQLLWKGSFKPSE 119

Query 121  NVKPLAPDNLTLHTNVSEWLLTWNLYPSNNLLYKDLISMVNISREDNPAEFIVYNTY 180
          +VKP AP NLT+HTNVSD LLTW+N YP +N LY L VNI E++PA+F +YNTY
Sbjct 120  HVKPRAPGNLTVHTNVSDTLLLTWSNPYPDPNYLNLTYAVNIWSENDPADFRIYNTY 179

Query 181  KEPRLSFPINILMSGVYYTARVRVRSQILTGTWSEWSPSITWYNHFLPLIQRPLGVTI 240
          EP L + L SG+ Y ARVR +Q TWSEWSPS W+N ++ P Q L LGV++
Sbjct 180  LEPSLRIAATLKSGISYRARVRAWAQCYNNTWSEWSPSTKWHNSYREPFEQHLLLGVS 239

Query 241  SCLCIPLFLCFYFSITKIKKIWWQIPTPARSPLVAIIIQDAQVPLWDKQTRSQUESTKY 300
          SC+ I CL CY SITKIKK WWDQIP PARS LVAIIIQDAQ W+K++R QE K
Sbjct 240  SCIVILAVCLLCYVSITKIKKEWWQIPNPARSRLVAIIIQDAQGSQWEKRSRQEPAC 299

Query 301  PHWKTCLDKLLPCLLKHVRKKKTDFFPKAAPTQSLQSPGKAGWCPMEVSRTVLWPENVS 360
          PHWK CL KLLPC L+H +K+ D KAA Q GK+ WCP+E+S+TVLWPE S+S
Sbjct 300  PHWKNCLTKLLPCFLEHNMKRDEDPHKAAKEMPFQSGKSAWCPVEISKTVLWPE--SIS 357

Query 361  VVRCMELFeapvqnveeeedeivkeDLSMSPENSGGCGFQESQADIMARLTENLFSDLLE 420
          VVRC+ELFEAPV+ EEEE E K SPE+S FQE + I+ARLTE+LF DLL
Sbjct 358  VVRCVELFEAPVECEEEEEVEEEKGSFCASPESSRD-DFQEGREGIVARLTESLFDLLG 416

Query 421  AENGGLGQSALAESCSPSPSGSQASVSWACLPMPGSEATCQVTEQPSH--PGPLSGSP 478
          ENGG Q + ESC PSGS A + W P +EA EQP H P P SP
Sbjct 417  EENGGFQCQDMGESCLLPSTGSAHMPWDEFPSAGPKEAPPWGKEQPLHLEPSP-PASP 475

Query 479  AQSAPTLACTQVPLVLADNPAYRSFSDCCSPAPNPGELAPEQQQADHLEEEPPSPADPH 538
          QS L CT+ PLV+A NPAYRSFS+ S +P P EL P+ A HLEE EP P P
Sbjct 476  TQSPDNLCTETPLVIAGNPAYRSFSNSLSQSPCPRELGPDPLLARHLEEEPEMPCVPQ 535

Query 539  SSGP---PMQPVESWEQILHMSVLQHgaagstapaggYQEFVQAVKQGAQDPGVPGV 595
          S P P E+WEQIL +VLQHGAAP AP GYQEFV AV+QG Q V G+
Sbjct 536  LSEPTTVPQPEPETWEQILRRNLVQHGAAPVSAPTSGYQEFVHAVEQGGTQASAVVGL 595

Query 596  RPSGDPGYKAFSSLLSSNGIRgdtaaagtdghggYKPFqnpvp----nqspssvpLFTF 651
          P G+ GYKAFSSLL+S+ + + G G GYKPFQ+ +P + +P VPLFTF
Sbjct 596  GPPGEAGYKAFSSLLASSAVSPEKCGFGASSGEEGYKPFQDLIPGCPGDPAPVPVPLFTF 655
```

Query 652 GLDTELSPLNSDPPKSPPEClglelglkggDWVKAPPPADQVPKPFGDDLGFIVYSS 711  
 GLD E SP +S P S PE LGLE G K D K P P +Q P D LG GIVYS+  
 Sbjct 656 GLDREPPRSPQSSHLPSSSPEHLGLEPGEKVEDMPKPPLPQEQATDPLVDSLCSGIVYSA 715

Query 712 LTCHLCGHLKQHHSQEEGGQSPIVASPGCGCCYDDRSPLGSLSGALESCPEGIPPEANL 771  
 LTCHLCGHLKQ H QE+GGQ+P++ASP CGCC DRS + A + P G+P EA+L  
 Sbjct 716 LTCHLCGHLKQCHGQEDGGQTPVMASPCCGCCCGDRSSPPTTPLRAPDPSPGGVPLEASL 775

Query 772 MSAPKTPSNLSGEGK-----GPGHSPVPSQTTEV 800  
 A PS +S + K PG++ SQT ++  
 Sbjct 776 CPASLAPSGISEKSKSSSSFHPAPGNAQSSSQTPKI 811

# IL-5 Receptor: 68%

>ref|NP\_000555.2| interleukin 5 receptor, alpha isoform 1 precursor [Homo sapiens]  
ref|NP\_783853.1| interleukin 5 receptor, alpha isoform 1 precursor [Homo sapiens]  
Length=420

GENE ID: 3568 IL5RA | interleukin 5 receptor, alpha [Homo sapiens]  
(Over 10 PubMed links)

Score = 584 bits (1505), Expect = 5e-167  
Identities = 285/414 (68%), Positives = 335/414 (80%), Gaps = 2/414 (0%)

Query	4	VLLILVGALATLQADLLNHKKFLLLPVNFTIKATGLAQVLLHWDPNPDQEQRHVDLEYH	63
		VLLIL+GA LQADLL +K LLPPVNFTIK TGLAQVLL W PNPDQEQR+V+LEY	
Sbjct	7	VLLIILGATEILQADLLPDEKISLLPPVNFTIKVTGLAQVLLQWKPNPDQEQRVNLEYQ	66
Query	64	VKINAPQEDEYDTRKTESKCVTPLHEGFAASVRTILKSSHTTLASSWVSaelKAPPGSPG	123
		VKINAP+ED+Y+TR TESKCVT LH+GF+ASVRTIL++ H+ LASSW SAEL APPGSPG	
Sbjct	67	VKINAPKEDDYETRITESKCVTILHKGFSASVRTILQNDHSSLASSWASaelHAPPGSPG	126
Query	124	TSVTNLTCtthtvssshthLRPYQVSLRCTLVVGKDAPEDTQYFLYYRFGVLTEKCQEYS	183
		TS+ NLCTT+T +++ LR YQVSL CTWLVG DAPEDTQYFLYYR+G TE+CQEYS	
Sbjct	127	TSIVNLCTTNTTEDNYSRLRSYQVSLHCTLVVGTDAPEDTQYFLYYRGSWTEECQEYS	186
Query	184	RDALNRNTACWFPRTFINSKGFEQLAVHINGSSKRAAIKPFQQLFSPLAIDQVNPPRNV	243
		+D L RN ACWFPRTFI SKG + LAV +NGSSK +AI+PFDQLF+ AIDQ+NPP NVT	
Sbjct	187	KDTLGRNIACWFPRTFILSKGRDWLAVLVNGSSKHSAIRPFDQLFALHAIDQINPPLNV	246
Query	244	VEIESNSLYIQWEKPLSAFPDHCfNYELKIYNTKNGHIQKEKLIANKFISKIDDVSTYSI	303
		EIE L IQWEKP+SAFP HCF+YE+KI+NT+NG++Q EKL+ N FIS IDD+S Y +	
Sbjct	247	AEIEGTRLSIQWEKPVSAFPIHCFDYEVKIHNRNGYLQIEKLMTNAFISIIDDLSKYDV	306
Query	304	QVRAAVSSPCRMpGRWGEWSQPIYVGK-ERKSLVEWHLIVLPTAACFVLLIFSLICRVCH	362
		QVRAAVSS CR G W EWSQPIYVG E K L EW +IV+ CF+LLI SLIC++CH	
Sbjct	307	QVRAAVSSMCREAGLWSEWSQPIYVGNDHKLREWFVIVIMATICFILLILSLICKICH	366
Query	363	LWTRLFPPVPAPKSNIKDLPVVTEYEKP-SNETKIEVVHCVEEVGFVGMNSTF	415
		LW +LFPP+PAPKSNIKDL V T YEK S+ET+IEV+ +E+ G E + +S F	
Sbjct	367	LWIKLFPPIPAPKSNIKDLFVTTNYEKAGSSETEIEVICYIEKPGVETLEDVSVF	420



Eotaxin Receptor: 70%

>ref|NP\_001828.1| CC chemokine receptor 3 [Homo sapiens]

ref|NP\_847899.1| CC chemokine receptor 3 [Homo sapiens]

Length=355

GENE ID: 1232 CCR3 | chemokine (C-C motif) receptor 3 [Homo sapiens]

(Over 10 PubMed links)

Score = 503 bits (1294), Expect = 1e-142

Identities = 244/348 (70%), Positives = 287/348 (82%), Gaps = 0/348 (0%)

```
Query 12  VESFETTPYEYEWAPPCEKVRKELGSWLLPPLYSLVFIIGLLGNMMVVLILIKYRKLQI 71
          VE+F TT Y + CEK + L + +PPLYSLVF +GLGN++VV+ILIKYR+L+I
Sbjct 8   VETFGTTSYDDVGLLCEKADTRALMAQFVPPPLYSLVFTVGLGNVVVVMILIKYRRLRI 67

Query 72  MTNIYLFNLAISDLLFLFTVPFVIHYVLWNEWGFGHYMCKMLSGFYLYALYSEIFFIILL 131
          MTNIYL NLAISDLLFL T+PFIHYV + W FGH MCK+LSGFY+ LYSEIFFIILL
Sbjct 68  MTNIYLLNLAISDLLFLVTLPFVIHYVRGNWVFGHGMCKLLSGFYHTGLYSEIFFIILL 127

Query 132 TIDRYLAIVHAVFALRARTVTFATITSIITWGLAGLAALPEFIFHESQDSFGEFSCSPRY 191
          TIDRYLAIVHAVFALRARTVTF ITSI+TWGLA LAALPEFIF+E+++ F E CS Y
Sbjct 128 TIDRYLAIVHAVFALRARTVTFGVITSIVTWGLAVLAALPEFIFYETEELFEETLCSALY 187

Query 192 PEGEEDSWKRPFHALRMNIFGLALPLLIMVICYSGIIKTLRCPNKKKKHAIRLifvmmiv 251
          PE SW+ FH LRM IF L LPLL+M ICY+GIKTLRCP+KKK+KAIRLIFV+M V
Sbjct 188 PEDTVYSWRHFHTLRMTIFCLVPLLVMAICYTGIKTLRCPSSKKKYKAIRLIFVIMAV 247

Query 252 fffFWTPYNLVLLFSAFHSTFLETSCQSKHLDLAMOQTEVIAYTHCCINPVIYAFVGEr 311
          FFIFFWTPYN+ +L S++ S C++SKHLDL M VTEVIAY+HCC+NPVIYAFVGER
Sbjct 248 FFIFFWTPYNVAILLSSYSILFGNDCERSKHLDLVMVTEVIAYSHCCMNPVIYAFVGER 307

Query 312 frkhlrlffhrNVAVYLGKYIPFLPGEKMERTSSVSPSTGEQEISVVF 359
          FRK+LR FFHR++ ++LG+YIPFLP EK+ERTSSVSPST E E+S+VF
Sbjct 308 FRKYLRFHFRHLLMHLGRYIPFLPSEKLERTSSVSPSTAEPELSIVF 355
```

PDGF  $\beta$  Receptor: 85%

>ref|NP\_002600.1| platelet-derived growth factor receptor beta precursor [Homo sapiens]  
Length=1106

GENE ID: 5159 PDGFRB | platelet-derived growth factor receptor, beta polypeptide [Homo sapiens] (Over 100 PubMed links)

Score = 1915 bits (4962), Expect = 0.0

Identities = 944/1106 (85%), Positives = 1021/1106 (92%), Gaps = 8/1106 (0%)

Query	1	MGLPGVIPAlvIrgql11-svlw11GPQTSRGLVITPPGPEFVLNISSTFVLTCSGSAPV	59
		M LPG +PAL L+G+LLL S+L LL PQ S+GLV+TPPGPE VLN+SSTFVLTCSGSAPV	
Sbjct	1	MRLPGAMPALALKGELLLL SLLLLLEPQISQGLVVTTPGPELVNVSSTFVLTCSGSAPV	60
Query	60	MWEQMSQVPWQEAAMNQDGTFFSSVLTLTNVTGGDTGEYFCVYNNSLGPELSERKRIYIFV	119
		+WE+MSQ P QE A QDGTFFSSVLTLTN+TG DTGEYFC +N+S G E ERKR+YIFV	
Sbjct	61	VWERMSQEPPEMAKAQDGTFFSSVLTLTNLTGLDTGEYFCTHNSRGLTDERKRLYIFV	120
Query	120	PDPTMGFLPMDSEDLFIFVTDVTETTIPCRVTD PQLEVTLHEKKVDIPLHVPYDHQRGFT	179
		PDPT+GFLP D+E+LFIF+T++TE TIPCRVTD PQ VTLHEKK D+ L VPYDHQRGF+	
Sbjct	121	PDPTVGFLPNDAEELFIFLTEITEITIPCRVTD PQLVTLHEKKGDVALPVPYDHQRGFS	180
Query	180	GT FEDKTYICKTTIGDREVSDTYVYVSLQVSSINVSNAVQTVVRQGESITIRCIVMGN	239
		G FED++YICKTTIGDREVSD YVYV LQVSSINVSNAVQTVVRQGE+IT+ CIV+GN	
Sbjct	181	GIFEDRSYICKTTIGDREVSDAYVYVRLQVSSINVSNAVQTVVRQGENITLMCIVIGN	240
Query	240	DVVNFQWYTPRMKSGRLVEPVDYLFQVPSRIGSILHIPTAELSDSGTYTCNVSVSNDH	299
		+VVNF+WYTPR +SGRLVEPVD+L +P I SILHIP+AEL DSGTYTCNV+ SVNDH	
Sbjct	241	EVVNFQWYTPRKESGRLVEPVD FLLDMPYHIRSILHIPS AELED SGTYTCNVTESVNDH	300
Query	300	GDEKAINISVIENG YVRLLET LGDVEIAELHRSRTL RVVFEAYPMP SVLWLDNRTL GDS	359
		DEKAINI+V+E+GYVRL +G ++ AELHRSRTL+VVFEAYP P+VLW KDNRTL GDS	
Sbjct	301	QDEKAINITVVESGYVRL LGVGT LQFAELHRSRTL QVVFEAYP PPTVLWFKDNRTL GDS	360
Query	360	GAGELVLSTRNMSETRYVSELILVRVKVSEAGYYTMRAFHEDEVLQSFKLQVNPVRVL	419
		AGE+ LSTRN+SETRYVSEL LVRVKV+EAG+YTMRAFHEDE VLQSF+LQ+NVPVRVL	
Sbjct	361	SAGEIALSTRNVSETRYVSELTLVRVKVAEAGHYTMRAFHEDEVLQSFQLQINVPVRVL	420
Query	420	ELSESH PANGEQT IRCRGRMPQPNVTWSTCRDLKRCPRKLSPTPLGNS SKEESQLETNV	479
		ELSESH P +GEQT+RCRGRMPQPN+ WS CRDLKRCPR+L PT LGNSS+EESQLETNV	
Sbjct	421	ELSESH PDSGEQTVRCRGRMPQPN IWSACRDLKRCPRELPPTLLGNSSEESQLETNV	480
Query	480	TFWEEDQEYEVVSTLRLRHVDQPLSVRCMLQNSMGDSQEVTVVPHSLPFKVVVISAILA	539
		T+WEE+QE+EVVSTLRL+HVD+PLSVRC L+N++G D+QEV VVPHSLPFKVVVISAILA	
Sbjct	481	TYWEEEQEFEVVSTLRLQHVD RPLSVRC LNAV GQDTQEVIVVPHSLPFKVVVISAILA	540
Query	540	lvvltvisliilimlwqkkpryeirwkviesvssdgheyiyvdpvqlpydstwelprdqL	599
		LVLVT+ISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDP+QLPYDSTWELPRDQL	
Sbjct	541	LVLVTIISLIILIMLWQKKPRYEIRWKVIESVSSDGHEYIYVDPMLPYDSTWELPRDQL	600
Query	600	VLGRTLGS GAFGQVVEATAHGLSHSQATMKVAVKMLKSTAR SSEQALMSELKIMSHLGP	659
		VLGRTLGS GAFGQVVEATAHGLSHSQATMKVAVKMLKSTAR SSEQALMSELKIMSHLGP	
Sbjct	601	VLGRTLGS GAFGQVVEATAHGLSHSQATMKVAVKMLKSTAR SSEQALMSELKIMSHLGP	660

Query	660	HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQRHSNKHCPPSAELYSNAL	719
		HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQ HS+K PPSAELYSNAL	
Sbjct	661	HLNVVNLLGACTKGGPIYIITEYCRYGDLVDYLHRNKHTFLQHSDKRRPPSAELYSNAL	720
Query	720	PVGFSPLSHLNLTGESDGGYDMSKDESIDYVPMLDMKGDIKYADIESPSYMAPYDNYVP	779
		PVG LPSH++LTGESDGGYDMSKDES+DYVPMLDMKGD+KYADIES +YMAPYDNYVP	
Sbjct	721	PVGLPLPSHVS LTGESDGGYDMSKDESVDYVPMLDMKGDVKYADIESSNYMAPYDNYVP	780
Query	780	SAPERTYRATLINDSPVLSYTDLVGFSYQVANGMDFLASKNCVHRDLAARNVLICEGKLV	839
		SAPERT RATLIN+SPVLSY DLVGFSYQVANGM+FLASKNCVHRDLAARNVLICEGKLV	
Sbjct	781	SAPERTCRATLINESPVLSYMDLVGFSYQVANGMEFLASKNCVHRDLAARNVLICEGKLV	840
Query	840	KICDFGLARDIMRDSNYISKGSTYLPWKMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	899
		KICDFGLARDIMRDSNYISKGST+LPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	
Sbjct	841	KICDFGLARDIMRDSNYISKGSTFLPLKWMAPESIFNSLYTTLSDVWSFGILLWEIFTLG	900
Query	900	GTPYPELPMNDQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFETRPPFSQlvlller	959
		GTPYPELPMN+QFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFE RPPFSQLVLLLER	
Sbjct	901	GTPYPELPMNEQFYNAIKRGYRMAQPAHASDEIYEIMQKCWEEKFEIRPPFSQLVLLLER	960
Query	960	llgegYKKKYQQVDEEFLRSDHPAILRSQARFPGIHSLRSPDTSVLYTAVQPNESDND	1019
		LLGEGYKKKYQQVDEEFLRSDHPAILRSQAR PG H LRSPLDTSVLYTAVQPN E DND	
Sbjct	961	LLGEGYKKKYQQVDEEFLRSDHPAILRSQARLPGFHGLRSPDTSVLYTAVQPNEGDND	1020
Query	1020	YIIPLDPKPDVADEGLPEGSPSLASSTLNEVNTSSTISCDSplelqeepp-----qa	1072
		YIIPLDPKPDVADEG EGSPSLASSTLNEVNTSSTISCDSPLE Q+EP+ Q	
Sbjct	1021	YIIPLDPKPEVADEGPLEGSPSLASSTLNEVNTSSTISCDSPLEQDEPEPEPQLELQV	1080
Query	1073	epeaqleqpqDSGCCPLAEADSFL	1098
		EPE +LEQ DSGCP P AEADSFL	
Sbjct	1081	EPEPELEQLPDGGCPAPRAEADSFL	1106

$\alpha$ V $\beta$ 3 Integrin: 92%

>ref|NP\_002201.1| integrin alpha-V precursor [Homo sapiens]  
Length=1048

GENE ID: 3685 ITGAV | integrin, alpha V (vitronectin receptor, alpha polypeptide, antigen CD51) [Homo sapiens] (Over 100 PubMed links)

Score = 1964 bits (5087), Expect = 0.0

Identities = 968/1049 (92%), Positives = 1008/1049 (96%), Gaps = 6/1049 (0%)

Query	1	MAApgrlllrprpggl1111pglllplADAFNLDVESPAEYAGPEGSYFGFAVDFFEPST	60
		MA P R LR P GL LLL GLLLPL AFNLDV+SPA EY+GPEGSYFGFAVDFF PS	
Sbjct	1	MAFPpRRRLRLGPRGLPLLLSGLLLPLCRAFNLVDSPA EYSGPEGSYFGFAVDFFVPSA	60
Query	61	SSRMFLLVGAPKANTTQPGIVEGGQVLKCECSSRRQCPIEFDSTGNRDYAKDDPLEFKS	120
		SSRMFLLVGAPKANTTQPGIVEGGQVLK+ SS+RRCQPIEFD+TGNRDYAKDDPLEFKS	
Sbjct	61	SSRMFLLVGAPKANTTQPGIVEGGQVLKCDWSSTRQCPIEFDATGNRDYAKDDPLEFKS	120
Query	121	HQWFGASVRSKQDKILACAPLYHWRTMKQEREPVGTCLQDGTCTVEYAPCRSKNIDAD	180
		HQWFGASVRSKQDKILACAPLYHWRTMKQEREPVGTCLQDGTCTVEYAPCRS++IDAD	
Sbjct	121	HQWFGASVRSKQDKILACAPLYHWRTMKQEREPVGTCLQDGTCTVEYAPCRSQDIDAD	180
Query	181	GQGFCCGGFSIDFTKADRVLLGGPGSFYWQGLISDQVAEIISKYDPNVYSIKYNNQLAT	240
		GQGFCCGGFSIDFTKADRVLLGGPGSFYWQGLISDQVAEI+SKYDPNVYSIKYNNQLAT	
Sbjct	181	GQGFCCGGFSIDFTKADRVLLGGPGSFYWQGLISDQVAEIVSKYDPNVYSIKYNNQLAT	240
Query	241	RTAQAIFFDSYLGYSVAVGDFNGDGIEDFVSGVPRAARTLGMVYIYDGKNMSSLHNFTGE	300
		RTAQAIFFDSYLGYSVAVGDFNGDGI+DFVSGVPRAARTLGMVYIYDGKNMSSL+NFTGE	
Sbjct	241	RTAQAIFFDSYLGYSVAVGDFNGDGIIDFVSGVPRAARTLGMVYIYDGKNMSSLYNFTGE	300
Query	301	QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRAVGDFQTTK	360
		QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRA GDFQTTK	
Sbjct	301	QMAAYFGFSVAATDINGDDYADVFIGAPLFMDRGSDGKLQEVGQVSVSLQRASGDFQTTK	360
Query	361	LNGFEVFARFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKKGLVYIFNGRSTGLNSVPSQI	420
		LNGFEVFARFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKKG+VYIFNGRSTGLN+VPSQI	
Sbjct	361	LNGFEVFARFGSAIAPLGDLDDQDGFNDIAIAAPYGGEDKKGIVYIFNGRSTGLNAVPSQI	420
Query	421	LEGQWAAQSMPPSFGYSMKGATDVDRNGYPDLVVGAFGVDRVLYRARPVTVNAGLEVY	480
		LEGQWAA+SMPPSFGYSMKGATD+D+NGYPDL+VGAFGVDR+LYRARPV+TVNAGLEVY	
Sbjct	421	LEGQWAARSMPSPFGYSMKGATDIDKNGYPDLIVGAFGVDRVLYRARPVITVNAGLEVY	480
Query	481	PSILNQDNKICPLPGTALKVSCFNVRFLKADGKGTLPKRLHFQVELLLDKLKQKGAIRR	540
		PSILNQDNK C LPGTALKVSCFNVRFLKADGKG LPRKL+FQVELLLDKLKQKGAIRR	
Sbjct	481	PSILNQDNKTCSLPGTALKVSCFNVRFLKADGKGVLPRKLNQVELLLDKLKQKGAIRR	540
Query	541	ALFLHNRSPPVHSKTMTVFRGGQMCEELVAYLRDESEFRDKLTPITIFMEYRLDQRTAAD	600
		ALFL++RSP HSK MT+ RGG MQCEEL+AYLRDESEFRDKLTPITIFMEYRLD RTAAD	
Sbjct	541	ALFLYSRSPSHSKNMTISRGGLMQCEELIAYLRDESEFRDKLTPITIFMEYRLDYRTAAD	600
Query	601	ATGLQPILNQFTPANVSRQAHILLDCGEDNVCKPKLEVSVNSDQKKIYIGDDNPLTLTVK	660
		TGLQPILNQFTPAN+SRQAHILLDCGEDNVCKPKLEVSV+SDQKKIYIGDDNPLTL VK	
Sbjct	601	TTGLQPILNQFTPANISRQAHILLDCGEDNVCKPKLEVSVSDQKKIYIGDDNPLTLIVK	660

Query	661	AQNQGEGAYEAEIIVSIPQADFIGVVRNNEALARLSCAFKTENQTRQVVCDLGNPMKAG	720
		AQNQGEGAYEAEIIVSIP QADFIGVVRNNEALARLSCAFKTENQTRQVVCDLGNPMKAG	
Sbjct	661	AQNQGEGAYEAEIIVSIPQADFIGVVRNNEALARLSCAFKTENQTRQVVCDLGNPMKAG	720
Query	721	TQLLAGLRFSVHQSEMDTSVKFDLQIQSSNSFDNVSPVVSVKVDLAVLAAVEIRGVSSP	780
		TQLLAGLRFSVHQSEMDTSVKFDL+IQSSN FD VSPVVS+KVDLAVLAAVEIRGVSSP	
Sbjct	721	TQLLAGLRFSVHQSEMDTSVKFDLQIQSSNLFDKVSPVVS HKVDLAVLAAVEIRGVSSP	780
Query	781	DHIFLPIPNWEYKENPETEEDVGPIVQHIYELRNNGPSSFSKAILNLQWPYKYNNTLLY	840
		DHIFLPIPNWE+KENPETEEDVGP+VQHIYELRNNGPSSFSKA+L+LQWPYKYNNTLLY	
Sbjct	781	DHIFLPIPNWEHKENPETEEDVGPVVQHIYELRNNGPSSFSKAMLHLQWPYKYNNTLLY	840
Query	841	ILHYDIDGPMNCTADTEINPLRIK-----TPEKNDTAAAGQGERNHLITKRDLTLREGDV	895
		ILHYDIDGPMNCT+D EINPLRIK T EKNDT AGQGER+HLITKRDL L EGD+	
Sbjct	841	ILHYDIDGPMNCTSDMEINPLRIKISSLOTTEKNDT-VAGQGERDHLITKRDLALSEGDI	899
Query	896	HTLGCGIAKCLQITCQVGRLDRGKSAILYVKSLLWTETFMNKENQNHYSYSLKSSASFNI	955
		HTLGCG+A+CL+I CQVGRLDRGKSAILYVKSLLWTETFMNKENQNHYSYSLKSSASFNI	
Sbjct	900	HTLGCGVAQCLKIVCQVGRLDRGKSAILYVKSLLWTETFMNKENQNHYSYSLKSSASFNI	959
Query	956	EFPPYKNLPIDLFNSTLVTTNITWGIQAPMPVPVWVVIILAVLAGLIIILAVLVFVMYRMG	1015
		EFPPYKNLPID+ NSTLVTTN+TWGIQAPMPVPVWVVIILAVLAGLIIILAVLVFVMYRMG	
Sbjct	960	EFPPYKNLPIDITNSTLVTTNVTWGIQAPMPVPVWVVIILAVLAGLIIILAVLVFVMYRMG	1019
Query	1016	FFKrvrppqeeqereqlqPHENGEGNSET	1044
		FFKRVRPPQEEQEREQLQPHENGEGNSET	
Sbjct	1020	FFKRVRPPQEEQEREQLQPHENGEGNSET	1048